

INFORMAL SEQUENCE LISTING

SEQ ID NOs: 9598-9600 and SEQ ID NO:9611 correspond to SEQ ID NOs: 1-3 and SEQ ID NO:14 of co-pending USSN _____, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US. The SEQ ID NOs. of this co-pending application USSN _____, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US, will be renumbered in a subsequent amendment as SEQ ID NOs: 9598- 10,466. For clarity, the SEQ ID NOs. in this continuation-in-part of USSN _____, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US. are numbered sequentially starting with SEQ ID NO:10,467.

SEQ ID NO:9598

LS 1384258.1 622 bp fragment of alternatively spliced variant of SEQ ID NO: 9600

INFORMATION FOR SEQ ID NO:9598:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA
<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9598:

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agagtgggtca gaggagaagt tgtatttgggt tgaaccttga aattaaaaat gatagaggaa 120
ttattatttgg gaccgttggt aggaataatg acttttccac tgcaagactg aagatatcag 180
tgccccctcta tattctgtgc aaaaggtgtc tttgactcat ccaaaaaatt gaacagtttc 240
ctgtctcatg gagatctatc acaaagtctt taaatattac tacccatgaa attggccagg 300
gttaggacat tcaaatgtct ttatccacat tcttgaagga taattgttat agattcccta 360
cctccatagg aatgcttata atggattatc tatacaatct ccacattccc acattttgca 420
ttagagaatg gaatcagtca aacctgttcc ccagagtttc ccttagagtt ctcacctgtt 480
gtcttatatc catctaggaa tccccatctc taatgtaagc ttggagatcc gggcccccg 540
gggacaggtg actgaaggac aaaaactgat cctgctctgc tcagtggctg aggggtacagg 600
aaatgtcaca ttctcctgggt ac 622
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SEQ ID NO:9599

"Ly1448" 523 bp cDNA fragment of alternatively spliced variant of SEQ ID NO: 9600

INFORMATION FOR SEQ ID NO:9599:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA

<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9599:

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ctgtcatgag gtctcttcta tagccatcag gtcttctcac agggatattc accaccttgc 60
tctggatagg cacatggccg ttgtcagctc tacagtaata tttgccggca tcaactctctt 120
tcacagctgg gatctccagc tctgctgaca gggaacgctg ggttttcttt ccataactgg 180
ttcctgtggc ctctctgtac caggagaatg tgacatttcc tgtaccccca gccactgagc 240
agagcaggat cagtttttgt ccttcagtca cctgtcccc gggggcccg atctccaagc 300
ttacattaga gatggggatt cctagatgga tataagacaa caggtagaaa ctctaaggga 360
aactctggga acagggtttg actgattcca ttctctaata caaaatgtgg gaatgtggag 420
attgtataga taatccatta taagcattcc tatggaggta gggaatctat aacaattatc 480
cttcaggaat gtggataaag acatttgaat gtcctaacc tgg 523
```

SEQ ID NO:9600: LS 368109.1 1908 bp full-length clone

INFORMATION FOR SEQ ID NO:9600:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA

<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9600:

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tgaggggctg ctcagcacc ttgnccagc caccgtggcc ttattatctt gctacggcct 120
caaaagaaaa ataggaagac gttcagccag ggatccactc aggagccttc ccagccctct 180
acccaagag ttcacctacc tcaactcacc taccacaggg cagctacagc ctatatatga 240
aaatgtgaat gttgtaagt gggatgaggt ttattcactg gcgtactata accagccgga 300
gcaggaatca gtagcagcag aaaccttggg gacacatatg gaggacaaga tgcagtcaact 360
gaacaggcag attcgtgac ccttgtggcg cctcttctg tcttcgaagg agacagcatc 420
gttctgaaat gccagggaga acagaactgg aaaattcaga agatggctta ccataaggat 480
aacaagagat tatctgtttt caagaaaatt ctcagatttc cttatccaaa gtgcagtgtt 540
aagtgcagat ggtaactatt tctgtagtac caaaggacaa ctcttctctt gggataaaac 600
ttcaaatata gtaaagatta aaagtccaag gaatccccat ctctaatagt agcttgagg 660
tccgggcccc cgggggacag gtgactgaag gacaaaaact gatcctgctc tgctcagtgg 720
ctgggggtac aggaaatgtc acattctcct ggtacagaga ggccacagga accagtatgg 780
gaaagaaaac ccagcgttcc ctgtcagcag agctggtaga tcccagctgt gaaagagagt 840
gatgccggca aatattactg tagagctgac aacggccatg tgcctatcca gagcaagggt 900
gtgaatatcc ctgtgagaat tccagtgtct cgccctgtcc tcaccctca ggtctcctgg 960
ggcccaggct gcagtggggg acctgctgga gcttactgt gaggccctg agaggtctc 1020
ccccaatctt gtaccaattt tatcatgagg atgtcaccct tgggaacagc tcggccctc 1080
tggaggaggg gctccttca acctctctt gactgcagaa cattctggaa actactcct 1140
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tgaggccaac aacggcctgg gggcccagtg caggtggagg gcagtgccag gtcctccatc 1200
 tcaggacctg atggctatag aaagagacct catgacagct ggagttctct ggggacctgt 1260
 ttggtgtcct tgcgttcact ggggtgttgc ttgctgttgc atgccttggt ccacaagata 1320
 tcaggagaaa gttctgccac taatgaaccc agaggggctt ccaggccaaa tcctcaagag 1380
 ttcacctatt caagcccaac cccagacatg gaggagctgc agccacgtgt atgtcaatgt 1440
 gggctctgta gatgtggatg tggtttattc tcaggctctgg agcatgcagc agccagaaaag 1500
 ctcagcaaac atcaggacac ttctggagaa caaggactcc caagtcatct actcttctgt 1560
 gaagaaatca taacacttgg aggaatcaga aggggaagatc aacagcaagg atggggcatc 1620
 attaagactt gctataaaac cttatgaaaa tgcttgaggc ttatcacctg ccacagccag 1680
 aacgtgcctc aggaggcacc tcctgtcatt tttgtcctga tgatgtttct tctccaatat 1740
 cttcttttac ctatcaatat tcattgaact gctgctacat ccagacactg tgcaataaaa 1800
 ttatttctgc taccttctct taagcaatca gtgtgtaaag atttgaggga agaatgaata 1860
 agagatacaa ggtctcacct tcactctactg tgaagtgatg agaacagg 1908

SEQ ID NO:9611: Ly1448 protein

INFORMATION FOR SEQ ID NO:9611:

(a) SEQUENCE CHARACTERISTICS:

<212> PRT

<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9611:

Met	Gly	Lys	Lys	Thr	Gln	Arg	Ser	Leu	Ser	Ala	Glu	Leu	Glu	Ile	Pro	5	10	15
Ala	Val	Lys	Glu	Ser	Asp	Ala	Gly	Lys	Tyr	Tyr	Cys	Arg	Ala	Asp	Asn	20	25	30
Gly	His	Val	Pro	Ile	Gln	Ser	Lys	Val	Val	Asn	Ile	Pro	Val	Arg	Ile	35	40	45
Pro	Val	Ser	Arg	Pro	Val	Leu	Thr	Leu	Arg	Ser	Pro	Gly	Ala	Gln	Ala	50	55	60
Ala	Val	Gly	Asp	Leu	Leu	Glu	Leu	His	Cys	Glu	Ala	Leu	Arg	Gly	Ser	65	70	75
Pro	Pro	Ile	Leu	Tyr	Gln	Phe	Tyr	His	Glu	Asp	Val	Thr	Leu	Gly	Asn	85	90	95
Ser	Ser	Ala	Pro	Ser	Gly	Gly	Gly	Ala	Ser	Phe	Asn	Leu	Ser	Leu	Thr	100	105	110
Ala	Glu	His	Ser	Gly	Asn	Tyr	Ser	Cys	Glu	Ala	Asn	Asn	Gly	Leu	Gly	115	120	125
Ala	Gln	Cys	Ser	Glu	Ala	Val	Pro	Val	Ser	Ile	Ser	Gly	Pro	Asp	Gly	130	135	140
Tyr	Arg	Arg	Asp	Leu	Met	Thr	Ala	Gly	Val	Leu	Trp	Gly	Leu	Phe	Gly	145	150	155
Val	Leu	Gly	Phe	Thr	Gly	Val	Ala	Leu	Leu	Leu	Tyr	Ala	Leu	Phe	His	165	170	175

Lys Ile Ser Gly Glu Ser Ser Ala Thr Asn Glu Pro Arg Gly Ala Ser
 180 185 190
 Arg Pro Asn Pro Gln Glu Phe Thr Tyr Ser Ser Pro Thr Pro Asp Met
 195 200 205
 Glu Glu Leu Gln Pro Val Tyr Val Asn Val Gly Ser Val Asp Val Asp
 210 215 220
 Val Val Tyr Ser Gln Val Trp Ser Met Gln Gln Pro Glu Ser Ser Ala
 225 230 235 240
 Asn Ile Arg Thr Leu Leu Glu Asn Lys Asp Ser Gln Val Ile Tyr Ser
 245 250 255
 Ser Val Lys Lys Ser
 260

SEQ ID NO:10,467: Ra12-Ly1464 fusion cDNA sequence (see, Example 7)

atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccaggggtggg 60
 cagggattcg ccattccgat cgggagggcg atggcgatcg cgggagagat caagcttccc 120
 accgttcata tcgggcttac cgccttccctc ggcttgggtg ttgtcgacaa caacggcaac 180
 ggcgacagag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
 ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
 gcgcttaacg ggcacatcat cgggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
 ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctccatggac 420
 atgaagctgg gctgtgtcct catggcctgg gccctctacc tttcccttgg tgtgtctctg 480
 gtggcccaga tgctactggc tgccagtttt gagacgtgc agtgtgaggg acctgtctgc 540
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 caggtcaagg cctacacttt cagtgaaccc ttccacctga ttgtgtccta tgactggctg 660
 atcctccaag gtccagccaa gccagttttt gaaggggacc tgctggttct gcgctgccag 720
 gcctggcaag actggccact gactcaggtg accttctacc gagatggctc agctctgggt 780
 cccccgggc ctaacaggga attctccatc accgtggtac aaaaggcaga cagcgggcac 840
 taccactgca gtggcatctt ccagagccct ggtcctggga tcccagaaac agcatctgtt 900
 gtggctatca cagtccaaga actgtttcca gcgccaatc tcagagctgt accctcagct 960
 gaaccccaag cagggaagccc catgaccctg agttgtcaga caaagttgcc cctgcagagg 1020
 tcagctgccc gcctcctctt ctcttctac aaggatggaa ggatagtgca aagcaggggg 1080
 ctctcctcag aattccagat cccacagct tcagaagatc actccgggtc atactggtgt 1140
 gaggcagcca ctgaggacaa ccaagtttgg aaacagagcc ccagctaga gatcagagt 1200
 caggtgtctt ccagctctgc tgcacctccc acattgaatc cagctcctca gaaatcagct 1260
 gctccaggaa ctgctcctga ggagggccct gggcctctgc ctccgcccgc aacctatct 1320
 tctgaggatc caggcttttc ttctcctctg gggatgccag atcctcatct gtatcaccag 1380
 atgggccttc ttctcaaaca catgcaggat gtgagagtc tccctcggtc cctgctcatg 1440
 gagttgaggg aattatctgg ccaccggaag cctgggacca caaaggctac tgctgaatag 1500

SEQ ID NO:10,468: Ra12-Ly1464 fusion amino acid sequence (see, Example 7)

Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 5 10 15
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala

35					40					45					
Phe	Leu	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val
50					55					60					
Gln	Arg	Val	Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr
65					70					75					80
Gly	Asp	Val	Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr
			85						90					95	
Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser
			100					105					110		
Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr
			115				120						125		
Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Ser	Met	Asp	Met	Lys	Leu	Gly
							135					140			
Cys	Val	Leu	Met	Ala	Trp	Ala	Leu	Tyr	Leu	Ser	Leu	Gly	Val	Leu	Trp
145							150					155			160
Val	Ala	Gln	Met	Leu	Leu	Ala	Ala	Ser	Phe	Glu	Thr	Leu	Gln	Cys	Glu
				165					170					175	
Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser	Cys	His	Thr	Glu	Asp	Asp	Leu
			180					185					190		
Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe	Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser
			195				200					205			
Glu	Pro	Phe	His	Leu	Ile	Val	Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly
							215					220			
Pro	Ala	Lys	Pro	Val	Phe	Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln
225							230					235			240
Ala	Trp	Gln	Asp	Trp	Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly
				245					250					255	
Ser	Ala	Leu	Gly	Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val
			260					265					270		
Val	Gln	Lys	Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln
			275				280					285			
Ser	Pro	Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr
			290				295					300			
Val	Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala
305							310					315			320
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	Leu
				325					330					335	
Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	Lys	Asp
			340					345					350		
Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	Gln	Ile	Pro
			355				360					365			

Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys Glu Ala Ala Thr
 370 375 380
 Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln Leu Glu Ile Arg Val
 385 390 395 400
 Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro Thr Leu Asn Pro Ala Pro
 405 410 415
 Gln Lys Ser Ala Ala Pro Gly Thr Ala Pro Glu Glu Ala Pro Gly Pro
 420 425 430
 Leu Pro Pro Pro Pro Thr Pro Ser Ser Glu Asp Pro Gly Phe Ser Ser
 435 440 445
 Pro Leu Gly Met Pro Asp Pro His Leu Tyr His Gln Met Gly Leu Leu
 450 455 460
 Leu Lys His Met Gln Asp Val Arg Val Leu Leu Gly His Leu Leu Met
 465 470 475 480
 Glu Leu Arg Glu Leu Ser Gly His Arg Lys Pro Gly Thr Thr Lys Ala
 485 490 495
 Thr Ala Glu

SEQ ID NO:10,469: LS 238330.1 (see, Example 9)

<210> 4
 <211> 1442
 <212> DNA
 <213> Homo sapiens

<400> 4
 gcgtgaggca ccgcggctgg cctgagtttc ttcttaatac tgtatcacaa ttgtgggctg 60
 tcttatgtgt tgatatcgat tgagctatth gaaataggaa tgtaaatggg tgtattaaat 120
 ttttgtaagg atataacaat atctaccttc caaggatggt gtgaggtttt ccatgatttt 180
 gtatatgagc taatgtttacc tttgaggggt ggtgtgcatt atgttggatg attgttaaatt 240
 ttcagtggaa aatgtaccgt gtcctaaatt taaagacatg aaaaatatcc caagatcata 300
 ctgatcata atagcaatth ctttacaaat gaattatgga ggtaactgat ctctaactgt 360
 ttccttcatg ttgttttaat gcacaagggc agaggatctg ctgacccttg gaaccagcgt 420
 gagctaacca cgtgctatag acacttcatg gtgtcgcacc caggggaagtc aaagcgcttt 480
 gctccctcac tgtctgtgag tctcagcca ttagtaccct acccccgct gctccaaaac 540
 ttgagttatt tcaaagtgtt ctactgttc atctctccac tgaccctact ccagaaagcc 600
 tggagagagt cccaagatgc caccacctt cccaatccc tggccacaga tctgtgtcta 660
 tctcacactc tgtaagtgcc gctttgcttc ttcctctctt gaaaagactg agaacacaca 720
 ttttaacatg ttaggaaaaat ggggcagcct aaaaaatgac tgatcccacc gccagtgact 780
 catgtatact ccaggctagc agacaaggcc ctttttggtg ggctgtctt tgtgggttca 840
 cagaaaccaa attactgtgg gttgcaaaga attagcaggc catttacaaa gcagacatcc 900
 cttcacccag actgtggttt tgcattgctc gggtctcagt ctatgagctt tgggtgcagga 960
 tcattttggc tactggaaaa accatagctt atttttaaatt tctgggtgcc aaagccacca 1020
 cacgtgtggt ctgtggatga ccattgtctg cagaatgacg aggaaggaac agaattgtgt 1080
 ttggggctca ggggtggcctt cccactggga ggggaaggcg gagggagccc ttgccctggg 1140
 ttttgacaca gccgtgtctc acagcctctc ctctcatctg catttctcag aaatgccctc 1200
 cctgcccagt ggtgactttt cctcgtcact cctatggagt tctacctgga gccagccat 1260
 gtgtggaact gtgaagttha ctctctgta aagatgggtt aaagaaagtc agcttctgaa 1320
 atgtaacaat gctaaccctt gctggaaccc tgtaagaaat agccttctg atagttttct 1380
 aggtttatca tgtttgattt ttacactgaa aaataaaaa atcctggtat gtttgaaaaa 1440
 aa 1442

SEQ ID NO:10,470: Ly1456P FL contig (see, Example 9)

<210> 5
<211> 1637
<212> DNA
<213> Homo sapiens

<400> 5
acctcctgagg ctcaagcaac gagccatcct cccgtcttag cctcccaact agctgagact 60
acaggcgtgg gtcaccacac ccagctaatt tttgtacttt ttgtagagac agggctctcac 120
catgttgccc aggctgggtcc tgaactcctg ggctcaagta atctgcccac ctcagcctcc 180
caaagtgttg gggttacagg cgtgaggcac cgcggctggc ctgagtttct tcttaatact 240
gtatcacaat tgtgggctgt cttatgtgtt gatatcgatt gagctatttg aaataggaat 300
gttaatgggt gtattaaatt tttgtaagga tataacaata tctaccttcc aaggatgttg 360
tgaggttttc catgattttg tatatgagct aatgttacct ttgaggggtg gtgtgcatta 420
tgttgatga ttgtaaattt tcagtggaaa atgtaccgtg tcctaaattt aaagacatga 480
aaaatatccc aagatcatac tagatcataa tagcaattcc ttacaaatg aattatggag 540
gtaactgatc tctaacagtt tccttcatgt tgttttaatg cacaagggca gaggatctgc 600
tgacccttgg aaccagcgtg agctaaccac gtgctataga cacttcatgg tgtcgacccc 660
agggaggtca aagcgttttg ctccctcact gtctgtgagt cctcagccat tagtacccca 720
cccccgctg ctccaaaact tgagttattt caaatgtttc tcaactgttca tctctccact 780
gacccactc cagaaagcct ggagagagtc ccaagatgcc acccaccttc cccaatccct 840
cgccacagat ctgtgtctat ctcacactct gtaagtgcgc ctttgcctct tcctctcttg 900
aaaagactga gaacacacat tttaacatgt taggaaaatg gggcagccta aaaaatgact 960
gatcccaccg ccagtgactc atgtatactc caggctagca gacaaggccc tttttggtgg 1020
gcctgcttct gtgggttcac agaaaccaa ttactgtggg ttgcaaagaa ttagcaggtc 1080
atttacaagg cagacatccc ttcacccaga ctgtggtttt gcatgctcag gttctcagtc 1140
tatgagcttt ggtgcaggat cattttggct actggaaaaa ccatagctta ttttaaattt 1200
ctgggtgcca aagccaccac acgtgtggtc tgtggatgac cattgtctgc agaatgacga 1260
ggaaggaca gaatgtggtt tggggctcag ggtggccttc ccactgggag ggaaggcggg 1320
agggagccct tgccctgggt tttgacacag cctgtgctca cagcctctcc tctcatctgc 1380
atttctcaga aatgccctcc ctgcccagtg gtgactttcc ctgctcactc ctatggagtt 1440
ctacctggag ccagccatg tgtggaactg tgaagtttac tcctctgtaa agatggttta 1500
aagaaagtca gcttctgaaa tgtaacaatg ctaacccttg ctggaaccct gtaagaaata 1560
gcctgctga tagttttcta ggtttatcat gtttgatttt tacactgaaa aataaaaaaa 1620
tcctgggtatg ttgaaa 1637

SEQ ID NO:10,471: Ly1456P FL contig ORF1 (see, Example 9)

<210> 6
<211> 98
<212> PRT
<213> Homo sapiens

<400> 6
Met His Lys Gly Arg Gly Ser Ala Asp Pro Trp Asn Gln Arg Glu Leu
5 10 15
Thr Thr Cys Tyr Arg His Phe Met Val Ser His Pro Gly Lys Ser Lys
20 25 30
Arg Phe Ala Pro Ser Leu Ser Val Ser Pro Gln Pro Leu Val Pro His
35 40 45
Pro Pro Leu Leu Gln Asn Leu Ser Tyr Phe Lys Cys Phe Ser Leu Phe
50 55 60
Ile Ser Pro Leu Thr Pro Leu Gln Lys Ala Trp Arg Glu Ser Gln Asp

65 70 75 80
 Ala Thr His Leu Pro Gln Ser Leu Ala Thr Asp Leu Cys Leu Ser His
 85 90 95
 Thr Leu

SEQ ID NO:10,472: Ly1456P FL contig ORF2 (see, Example 9)

<210> 7
 <211> 59
 <212> PRT
 <213> Homo sapiens

 <400> 7
 Met Phe Leu Thr Val His Leu Ser Thr Asp Pro Thr Pro Glu Ser Leu
 5 10 15

 Glu Arg Val Pro Arg Cys His Pro Pro Ser Pro Ile Pro Arg His Arg
 20 25 30

 Ser Val Ser Ile Ser His Ser Val Ser Ala Ala Leu Leu Leu Pro Leu
 35 40 45

 Leu Lys Arg Leu Arg Thr His Ile Leu Thr Cys
 50 55

SEQ ID NO:10,473: Ly1456P FL contig ORF3 (see, Example 9)

<210> 8
 <211> 84
 <212> PRT
 <213> Homo sapiens

 <400> 8
 Met Thr Ile Val Cys Arg Met Thr Arg Lys Glu Gln Asn Val Val Trp
 5 10 15

 Gly Ser Gly Trp Pro Ser His Trp Glu Gly Arg Arg Glu Gly Ala Leu
 20 25 30

 Ala Leu Gly Phe Asp Thr Ala Cys Ala His Ser Leu Ser Ser His Leu
 35 40 45

 His Phe Ser Glu Met Pro Ser Leu Pro Ser Gly Asp Phe Pro Ser Ser
 50 55 60

 Leu Leu Trp Ser Ser Thr Trp Ser Pro Ala Met Cys Gly Thr Val Lys
 65 70 75 80

 Phe Thr Pro Leu

SEQ ID NO:10,474: Ly1456P FL contig ORF4 (see, Example 9)

<210> 9
 <211> 66
 <212> PRT

<213> Homo sapiens

<400> 9

Met Trp Phe Gly Ala Gln Gly Gly Leu Pro Thr Gly Arg Glu Gly Gly
5 10 15
Arg Glu Pro Leu Pro Trp Val Leu Thr Gln Pro Val Leu Thr Ala Ser
20 25 30
Pro Leu Ile Cys Ile Ser Gln Lys Cys Pro Pro Cys Pro Val Val Thr
35 40 45
Phe Pro Arg His Ser Tyr Gly Val Leu Pro Gly Ala Gln Pro Cys Val
50 55 60
Glu Leu
65

SEQ ID NO:10,475:

GenBank clone on chromosome 15q21 clone b2265b18 (acc. no. AC008131)

see Figure 24 for sequence

SEQ ID NO:10,476

human secreted protein-encoding gene 9 cDNA clone HTOHB55 SEQ ID NO:1 (acc. no. AAH19210)

see Figure 25 for sequence

SEQ ID NO:10,477

human secreted protein-encoding gene 9 cDNA clone HTOHB55 SEQ ID NO:19 (acc. no. AAH19178) on chromosome 15q21

see Figure 26 for sequence

SEQ ID NO:10,478

lung cancer associated polynucleotide sequence SQID 265 (Genseq accession number AAF18246)

see Figure 29 for sequence

SEQ ID NO:10, 479

homo sapiens Genbank clone on chromosome 17 clone RP11-956N15 (accession number AC021581)

see Figure 30 for sequence

SEQ ID NO:10,480: Template LS 1076101.8 HERV nucleotide sequence

(see, Example 11)

gccgctgccg ctccaggaga caggttccca tgcaggaatg aaagacatgg aaggggaagag 60
ggggggccagc tccctgagtc ctgtgtccac cagctgctgc taaatacctc tgagaaactc 120
tgcttctatc taagggggacc tacttctctc gggaatctca atacttgga caagaacctc 180
ctagacggac cctttggcat aatgaattgg accaactgta ggttccagga ctagagagcc 240
agcaatgcct ccatgaacaa tctcacccaa ttactctgct caggaaacga ggtaactgat 300
ggacagccga ggcagcccct taggcggcctt aggcctcccc tgtggagcat ccctgaggcg 360
gactccggcc agcccagtg atgcatcca aagagcactc ccgggtagga aattgccccg 420
gtggaatgcc tcaccagagc agcgtgtagc agttccctgt ggaggattaa cacagtggct 480
gaacaccggg aaggaactgg cacttggagt ccggacatct gaaacttgta gactgggagc 540
tgtacatgga tgggagcagc ttcaccaacc cctgcaaagt gactctgaag aagacgacaa 600
gccctgctcc agtcacaccc ggaagctgac tgggtccacgc acagctgaag catgaggaaa 660
ctcatcgagg gactaatttt ccttaaaatt tagacttgca cagtaaggac ttcaactgac 720
cttctcaga ctgagaactg tttccagtat atacatcaag tcaactgaggt aggacaaaag 780
attgctacat tcctattatt ttaaggttac atttttgggg acccctcttt cttctgttct 840
agctattacc tttctgtgt cacttagaaa aggaccagtc cttaattgta ttttaaaaac 900
tgtgatcatg ggaagcttta aattggttca ataacacgca tcaagttggt tatttctctg 960
gctacatacc ttgatagat 980

SEQ ID NO:10,481: Template LS 1076101.8 HERV amino acid sequence

(see, Example 11)

Met Asp Ser Arg Gly Ser Pro Leu Gly Gly Leu Gly Leu Pro Cys Gly
5 10 15
Ala Ser Leu Arg Arg Thr Pro Ala Ser Pro Ser Asp Ala Ile Gln Arg
20 25 30
Ala Leu Pro Gly Arg Lys Leu Pro Arg Trp Asn Ala Ser Pro Glu Gln
35 40 45
Arg Val Ala Val Pro Cys Gly Gly Leu Thr Gln Trp Leu Asn Thr Gly
50 55 60
Lys Glu Leu Ala Leu Gly Val Arg Thr Ser Glu Thr Cys Arg Leu Gly
65 70 75 80
Ala Val His Gly Trp Glu Gln Leu His Gln Pro Leu Gln Ser Asp Ser
85 90 95
Glu Glu Asp Asp Lys Pro Cys Ser Ser His Thr Arg Lys Leu Thr Gly
100 105 110
Pro Arg Thr Ala Glu Ala
115

SEQ ID NO:10,482: LS-1452 with His tag nucleotide sequence (see, Example 13)

atgcagcatc accaccatca ccacgtgtca caatctacag tcaggcagga ttctcctgtg 60
gagccctggg aagggatcag cgatcactct ggcattattg atggttcgcc cagactcctg 120
aacactgacc atcctccttg ccaattagac atcaggtctc tgaggcacia agctgtctgg 180
attaaccccc aggatgtgca gcaacagccg caggacttgc aatctcaggt gccagcagca 240

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gggaacagtg ggacccattt tgtgacagat gctgcctctc cctcaggccc ttcaccttcg 300
tgctcggggg actccctggc agagacaacg ttgtctgagg ataccacaga ctccgttggc 360
agcgcttctc cccatggctc gagtgaaaag agtagcagct tctctctgtc ctcaacagag 420
gtacacatgg tccgcccagg atactctcat cgggtgtctc tgcccacaag ccctgggatt 480
ttggccacct ccccatatcc tgagactgac agtgcttttt ttgagccttc ccatctgaca 540
tctgctgctg atgaagggtc tgttcaagtc agtagaagaa ccatttcttc gaattccttc 600
tcaccagagg tatttgtgct gcctgttgat gtagaaaagg aaaatgccc cttttatgtt 660
gcagatatga ttatatcagc aatggagaaa atgaagtgtg acattctgag tcaacagcag 720
acagagagct ggagtaaaga agtcagtggg ttacttggga gtgatcagcc tgactctgaa 780
atgacttttg ataccaacat aaagcaagag tctgggtctt ctacttcttc atacagtggc 840
tatgaagggt gtgctgtgtt acaggtcagc ccagtgtactg aaacacgtac ttaccatgat 900
gtgaaagaga ttgcaaagt cgatgttgat gaatttgta ttttagagct tggagatttt 960
aatgatatac cagaaacctg tagctgttcc tgcagctcct ctaagagtgt cacttatgag 1020
ccagacttca attctgcaga actattagcc aaagagctgt accgcgtgtt ccagaagtgc 1080
tggatactgt cagtagttaa ttctcagctg gcaggttccc tgagtgcagc tggctcgata 1140
gtcgtaaatg aagagtgtgt ccgaaaagac tttgaatcca gtatgaatgt agtacaggaa 1200
attaaattta agtctaggat cagagggact gaagactggg ctctctctag atttcaaadc 1260
atatttaata ttcattccacc actcaagagg gaccttgtgg tggcagccca gaattttttc 1320
tgtgccggct gtggaactcc agtagagcct aagtttgtga agcggctccg gtactgcgaa 1380
tacctaggga agtatttctg tgactgtgct cactcatatg cagagtctgt catccctgcc 1440
cgaatcctga tgatgtggga cttcaagaag tactacgtca gcaatttctc caaacagctg 1500
ctcgacagca tatggcacca gccatttttc aatttgtgta gcatcggcca aagcctgtat 1560
gcgaaagcca aggagctgga cagagtgaag gaaattcagg agcagctctt ccatatcaag 1620
aagctgttga agacctgtag gtttgctaac agtgcattaa aggagtctga gcagggtgccg 1680
ggacacttga ctgatgagct ccacctgttc tcccttgagg acctggctag gatcaagaaa 1740
gggctgctgg cacccttact caaggacatt ctgaaagctt cccttgacac tgtggctggc 1800
tgtgagctgt gtcaaggaaa gggctttatt tgtgaatttt gccagaatac gactgtcatc 1860
ttcccatctc agacagcaac atgtagaaga tgttcagcgt gcagggtctg ctttcacaaa 1920
cagtgtcttc agtcctccga gtgcccccg tgtgagagga tcacagcgag gagaaaactt 1980
ctggaaagtg tggcctctgc agcaaca 2007

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SEQ ID NO:10,483: LS-1452 with His tag amino acid sequence (see, Example 13)

```

Met Gln His His His His His Val Ser Gln Ser Thr Val Arg Gln
                    5              10              15
Asp Ser Pro Val Glu Pro Trp Glu Gly Ile Ser Asp His Ser Gly Ile
                20              25              30
Ile Asp Gly Ser Pro Arg Leu Leu Asn Thr Asp His Pro Pro Cys Gln
                35              40              45
Leu Asp Ile Arg Leu Met Arg His Lys Ala Val Trp Ile Asn Pro Gln
                50              55              60
Asp Val Gln Gln Gln Pro Gln Asp Leu Gln Ser Gln Val Pro Ala Ala
                65              70              75              80
Gly Asn Ser Gly Thr His Phe Val Thr Asp Ala Ala Ser Pro Ser Gly

```

	85	90	95
Pro Ser Pro Ser Cys Leu Gly Asp Ser Leu Ala Glu Thr Thr Leu Ser			
	100	105	110
Glu Asp Thr Thr Asp Ser Val Gly Ser Ala Ser Pro His Gly Ser Ser			
	115	120	125
Glu Lys Ser Ser Ser Phe Ser Leu Ser Ser Thr Glu Val His Met Val			
	130	135	140
Arg Pro Gly Tyr Ser His Arg Val Ser Leu Pro Thr Ser Pro Gly Ile			
	145	150	155
Leu Ala Thr Ser Pro Tyr Pro Glu Thr Asp Ser Ala Phe Phe Glu Pro			
	165	170	175
Ser His Leu Thr Ser Ala Ala Asp Glu Gly Ala Val Gln Val Ser Arg			
	180	185	190
Arg Thr Ile Ser Ser Asn Ser Phe Ser Pro Glu Val Phe Val Leu Pro			
	195	200	205
Val Asp Val Glu Lys Glu Asn Ala His Phe Tyr Val Ala Asp Met Ile			
	210	215	220
Ile Ser Ala Met Glu Lys Met Lys Cys Asn Ile Leu Ser Gln Gln Gln			
	225	230	235
Thr Glu Ser Trp Ser Lys Glu Val Ser Gly Leu Leu Gly Ser Asp Gln			
	245	250	255
Pro Asp Ser Glu Met Thr Phe Asp Thr Asn Ile Lys Gln Glu Ser Gly			
	260	265	270
Ser Ser Thr Ser Ser Tyr Ser Gly Tyr Glu Gly Cys Ala Val Leu Gln			
	275	280	285
Val Ser Pro Val Thr Glu Thr Arg Thr Tyr His Asp Val Lys Glu Ile			
	290	295	300
Cys Lys Cys Asp Val Asp Glu Phe Val Ile Leu Glu Leu Gly Asp Phe			
	305	310	315
Asn Asp Ile Thr Glu Thr Cys Ser Cys Ser Cys Ser Ser Ser Lys Ser			
	325	330	335
Val Thr Tyr Glu Pro Asp Phe Asn Ser Ala Glu Leu Leu Ala Lys Glu			
	340	345	350
Leu Tyr Arg Val Phe Gln Lys Cys Trp Ile Leu Ser Val Val Asn Ser			
	355	360	365
Gln Leu Ala Gly Ser Leu Ser Ala Ala Gly Ser Ile Val Val Asn Glu			
	370	375	380
Glu Cys Val Arg Lys Asp Phe Glu Ser Ser Met Asn Val Val Gln Glu			
	385	390	395
Ile Lys Phe Lys Ser Arg Ile Arg Gly Thr Glu Asp Trp Ala Pro Pro			
	405	410	415
Arg Phe Gln Ile Ile Phe Asn Ile His Pro Pro Leu Lys Arg Asp Leu			
	420	425	430
Val Val Ala Ala Gln Asn Phe Phe Cys Ala Gly Cys Gly Thr Pro Val			
	435	440	445

Glu Pro Lys Phe Val Lys Arg Leu Arg Tyr Cys Glu Tyr Leu Gly Lys
450 455 460
Tyr Phe Cys Asp Cys Cys His Ser Tyr Ala Glu Ser Cys Ile Pro Ala
465 470 475 480
Arg Ile Leu Met Met Trp Asp Phe Lys Lys Tyr Tyr Val Ser Asn Phe
485 490 495
Ser Lys Gln Leu Leu Asp Ser Ile Trp His Gln Pro Ile Phe Asn Leu
500 505 510
Leu Ser Ile Gly Gln Ser Leu Tyr Ala Lys Ala Lys Glu Leu Asp Arg
515 520 525
Val Lys Glu Ile Gln Glu Gln Leu Phe His Ile Lys Lys Leu Leu Lys
530 535 540
Thr Cys Arg Phe Ala Asn Ser Ala Leu Lys Glu Phe Glu Gln Val Pro
545 550 555 560
Gly His Leu Thr Asp Glu Leu His Leu Phe Ser Leu Glu Asp Leu Val
565 570 575
Arg Ile Lys Lys Gly Leu Leu Ala Pro Leu Leu Lys Asp Ile Leu Lys
580 585 590
Ala Ser Leu Ala His Val Ala Gly Cys Glu Leu Cys Gln Gly Lys Gly
595 600 605
Phe Ile Cys Glu Phe Cys Gln Asn Thr Thr Val Ile Phe Pro Phe Gln
610 615 620
Thr Ala Thr Cys Arg Arg Cys Ser Ala Cys Arg Ala Cys Phe His Lys
625 630 635 640
Gln Cys Phe Gln Ser Ser Glu Cys Pro Arg Cys Ala Arg Ile Thr Ala
645 650 655
Arg Arg Lys Leu Leu Glu Ser Val Ala Ser Ala Ala Thr
660 665

SEQ ID NO:10,484: TCL-1 with His tag nucleotide sequence (see, Example 13)

atgcagcatc accaccatca ccacgccgag tgcccgcacac tcggggaggc agtcaccgac 60
caccgcgacc gcctgtgggc ctgggagaag ttcgtgtatt tggacgagaa gcagcacgcc 120
tggtgcct taaccatcga gataaaggat aggttacagt tacgggtgct cttgcgtcgg 180
gaagacgtcg tcctggggag gcctatgacc cccaccaga taggccaag cctgctgcct 240
atcatgtggc agctctaccc tgatggacga taccgatcct cagactccag tttctggcgc 300
ttagtgatcc acatcaagat tgacggcgtg gaggacatgc ttctcgagct gctgccagat 360
gactgatga
369

SEQ ID NO:10,485: TCL-1 with His tag amino acid sequence (see, Example 13)

Met Gln His His His His His His Ala Glu Cys Pro Thr Leu Gly Glu
5 10 15
Ala Val Thr Asp His Pro Asp Arg Leu Trp Ala Trp Glu Lys Phe Val
20 25 30

Tyr Leu Asp Glu Lys Gln His Ala Trp Leu Pro Leu Thr Ile Glu Ile
 35 40 45
 Lys Asp Arg Leu Gln Leu Arg Val Leu Leu Arg Arg Glu Asp Val Val
 50 55 60
 Leu Gly Arg Pro Met Thr Pro Thr Gln Ile Gly Pro Ser Leu Leu Pro
 65 70 75 80
 Ile Met Trp Gln Leu Tyr Pro Asp Gly Arg Tyr Arg Ser Ser Asp Ser
 85 90 95
 Ser Phe Trp Arg Leu Val Tyr His Ile Lys Ile Asp Gly Val Glu Asp
 100 105 110
 Met Leu Leu Glu Leu Leu Pro Asp Asp
 115 120

Sequences Listed in Figure 5- Highly expressed in lymphoma cells

SEQ ID NO: 10,486

gtgaaacacc ctcgccggg aagtcagttc gttctctcct ctctctctct cttgtttgaa 60
 catggtgcgg actaaagcag acagtgttcc aggcacttac agaaaagtgg tggctgctcg 120
 agccccaga aaggtgcttg gttcttccac ctctgccact aattcgacat cagtttcatc 180
 gaggaagct gaaaataaat atgcaggagg gaaccccggt tgcgtgcgcc caactcccaa 240
 gtggcaaaaa ggaattggag aattctttag gttgtcccct aaagattctg aaaaagagaa 300
 tcagattcct gaagaggcag gaagcagtggt cttaggaaaa gcaaagagaa aagcatgtcc 360
 tttgcaacct gatcacacaa atgatgaaaa agaatagaac tttctcattc atctttgaat 420
 aacgtctcct tgtttaccct ggtattctag aatgtaaatt tacataaatg tgtttgttcc 480
 aattagcttt gttgaacagg catttaatta aaaaatttag gttt 524

SEQ ID NO: 10,487

ctgcttgtag ttcaaagccc tccgtctagc catctcagcc aggtcaggt tccttctccc 60
 acccatcagg ccaagcagga cttgtcaaac atacacattc aagttcctag cacacagtag 120
 gtgctaagt ggaattgatt ataaacttga attcttccat caacaaatat ccacctctcc 180
 tgtccagctt gcctcagatc ttcaggttct ctcttctctg aggcagctaa gcttctacat 240
 ccttcatgaa gtttccttta cttctcgaca gaagacagtt ccctttagg 289

SEQ ID NO: 10,488

ccattagctc ctgtagctag ttctgtctt ttccaaaacc tggttttttt ttggcttttt 60
 ggtagatgct gtggctctct tatggcctcc aataaacata agtgaggcag agttgggttt 120
 tattgtttgc aaccaacgaa cttaattgat tctgtattag aaagaactgg tatatttctt 180
 taagcaaaga ctaggactct atgggggtca acaaactctg taatcgctt tccactcccc 240
 tggacaaaat aaatatattg tctactgctg aaacgcaaat tatccccaaa ccaagtagct 300
 tt 302

SEQ ID NO: 10,489

tataaactgt ggcgggatag ttttcgggtc cttgtccagt gaaacacct cgccggggaa 60
 gtcagttcgt tctctcctct cctctcttct tgtttgaaca tgggtgcggac taaagcagac 120
 agtggtccag gcacttacag aaaagtgggt gctgctcgag cccccagaaa ggtgcttggt 180
 tcttccacct ctgccactaa ttcgacatca gtttcatcga ggaaagctga aaataaatat 240
 gcaggaggga accccggttg cgtgcgcccc actcccaagt ggcaaaaagg aattggagaa 300
 ttcttttaggt tgtcccctaa agattctgaa aaagagaatc agattcctga agaggcagga 360
 agcagtggtc taggaaaaagc aaagagaaaa gcatgtcctt tgcaacctga tcacacaaat 420

gatgaaaaag aatagaactt tctcattcat ctttgaataa cgtctccttg tttaccctgg 480
tattctagaa tgtaaattta cataaatgtg tttgttccaa ttagctttgt tgaacaggca 540
tttaattaaa aaatttaggt tt 562

SEQ ID NO: 10,490

ctgcttggac ttcaaagccc tccgcctagc catctcagcc aggetcaggt tccttctccc 60
acccatcagg ccaagcagga cttgtcaaac atacacattc aagttcctag cacacagtag 120
gtgctaagt ggaattgatt ataaacttga attcttccat caacaaatat ccacctctcc 180
tgtccagctt gcctcagatc ttcaggttct ctcttctctg aggcagctaa gcttctacat 240
ccttcagtaa gtttctctta cttctcgaca gaagacaggt ccctttagg 289

SEQ ID NO: 10,491

aaaaaaaaa aacaaagcaa agcaaagcaa aacaaaacag ctctttataa tgtacaatgg 60
cttaagcaaa tcgcttttagt tttttttcta ttttaagattt aggacagact actcgtctaa 120
aattcactat ttacagagaa ggtcctaggg aacaggataa cttatttagg tttagctctc 180
ataatacaat atccataatg gctttagaag aatgtaaata aataacattg gtaaacagcg 240
tatactgata ttttctgaca aactcattta tctaactca tgctgagcaa tcaagaggat 300
tcctctatat atttt 315

SEQ ID NO: 10,492

aaaaaaaaa tcaaaagcag acatgttttg ctgaaataaa accaagaaac acagctaaaa 60
ctccccata aacctaaaag tccatggaga attcaatttc tcatttccat tcagaaatct 120
ggctacaaag tgatttggtt gctatttggtg acagtacaga gtgctgaaag aaaccagct 180
cttgagtctc ttagatccca tcctgtagga agtggtggga aagccagcgg accatgggca 240
agtcaactcc tggtacttg gcagggagtc agactgtgct ctctccattc cccaggactc 300
cacagaacca tctggtactg ctagtgtctg gtgaacagt agagcagagt ccacaaaacg 360
cagagaacca gaatgtgacc gcaaggagcc aggacctgt gctttttcat ggattacaaa 420
tctagggcca aggagaggga aagcagaaa agccctattg ggaagaggag ctggctgcgc 480
ccctaaactg agatggaaa agtaaggctc ttgagccac acctgg 526

SEQ ID NO: 10,493

ctgggcaana ccaagtcaca gtttccagcg tgctgtctag ccctccgagt gtgtgtgctc 60
atccttttca tagaagtccc atmkgscatg gagagggttg ggctgcarag ctgwgattgc 120
cagaggccct tccttgagaa ctgtggggaa ggaggccctg ggggtttctt ctgtaggcag 180
agctcaggcc ccagtcacct ctgccacct cagcctggca ctgttggtgc agagcctctg 240
ctgcctctct ctctctaccc atctgcagac cagcagaata ttctccccct ctcacacca 300
accaggagtt tggtgtggtt tctggacacg gccagagcag tcactgcggg gctggttttg 360
ctgggcttcc ctgtcaaagc aatgctaacg tccagctctc gactcaaggc caggttcttc 420
tcccacttgt ggctcttggt gcttgagggc tgagccagg gctcctctcc tgctggccgt 480
ccaggaacag acatcttcac atcctcagtc ttccaaaccc ggacctgccc gtcttgactc 540
ccggtgatga tgatctggct tgtgtcccat gctgggccct ccatcaggca gcaacagggt 600
atggctcctt ctgggccccca ggctgtggtg atgctgg 637

SEQ ID NO: 10,494

aaacaatgct acactcattt ttggcaaagt gctgtattgt tcagtctgtg tacaaaactg 60
accatctatg aaccaatcag tataaaaaat ttctataaaa acaaaattta gacagtggct 120
caagaaaaca agctgccatt tatgcataga ttgatgtaca gtaacctaac caaatgtccc 180
ttttgaattt tcaagttact gaaaaaaaaa gtgtcgagaa acacattaag aaggcacatg 240
tacagtctac aatactcttc agtctcccta actcatgcc tgcccctata aaggaaatat 300
gttcacaatt ttacttgaga aaaaaaaaaa aagccactta aaaaaaaaaa acacacacgc 360
aattattaaa gttcaaaatc tctggaggaa aatacaagca aaaccactca tacactccaa 420
gcctgaaaca cacatctaac ctccccaggt actggtttgg ttttcagagg tccacctana 480
aaacaaatac taaaacttca ggcaaaacag agcaaaactg gacatttaac aattacacaa 540

ttttt

545

SEQ ID NO: 10,495

ctgaataggc	acccaaaagt	ccgtgactaa	atttcgtttg	tctttttgat	agcaaattat	60
gttaagagac	agtgatggct	agggctcaac	aattttgtat	tcccatgttt	gtgtgagaca	120
gagtttgttt	tcccttgaac	ttgggttagaa	ttgtgctact	gtgaacgctg	atcctgcata	180
tggaagtccc	gcttcggtga	catttcctgg				210

SEQ ID NO: 10,496

cctcctcgac	caaggcaggg	aacttcaatc	tgtataagta	tctgcagttg	ctggaataat	60
ttgaagaccc	catggagcta	aggagattaa	gtggaggatt	ttcattgttt	cagaggggca	120
aggggcaaat	ccattgctaa	ttctttaatg	atgaaaaatg	gtaagaagtt	gttaaaactcc	180
tttggggatt	ttaaaaagtg	atacgtaaac	agaagagaga	gagagagaga	gaaatcacag	240
tagtgaggct	aacaaaaata	atgataaaaa	ggttagaaga	accaggata	cttagtggat	300
gcctagacaa	cataaaaaata	gatttataga	aggaagcaat	ggaatttgaa	tataaaaggg	360
tatcagaaaag	ttaatgtgtt	gcatctgaaa	ttcaaagtat	ttccttttgg	ctacacaaga	420
aagactttta	ataaaaccct	ttgtatatat	ttctgaaagg	naaatatttt	ataggggaaat	480
ggaggattgg	aagaaaatct	gttccatcat	gtctgggtat	tagaattttg	cttaataact	540
tgccaaaata	ttacgcttcc	aagggtcatg	gcattatgtg	tgtaccaaat	taaag	595

SEQ ID NO: 10,497

ctgtggctgt	ctgtcagaga	agcacatttt	tctgcagata	attagaatgg	cttcccccat	60
ctctcacgga	ctgtcccaag	tctagaaaag	aattgagttc	ctcttctatt	agtcaataaa	120
aagggaagag	aatgtttgtc	ttcctttcct	ttctgtagtg	ttaagaaaat	aaacgaactt	180
aatgattcta	aattatcagt	gagcttaaca	ctgtactata	gaccaaagat	taccttttca	240
aaaagtccct	tgagggtgaaa	tattttgtat	acgtaataca	tagatgcaca	tataaacaca	300
cacatataga	atctcaatat	tttaacactt	ctttgggtag	ttgtactaac	tcactaaccc	360
tgaggaaaaa	gttaagaaat	tgaaagtgtt	ttcttcaaaa	gttgagattt	aacaataaaa	420
gggtgttactt	tgataactaa	aaggaaacttt	attatcctct	tcctaaaata	aaccaatgcc	480
tattctgaaa	atggcacttg	caattacaat	ttgccattat	caaagctacc	actgaggtag	540
aggcattatc	taaaacaaat	accacttatc	atattattggc	agttacctcg	agagagaccc	600
atacaccatc	ttctagcaga	gcacagtcaa	tcaaattacc	ttcgggtaaa	gctatagcat	660
gtctagtctg	ttgacagata	ttaaagggtg	tcataaaaga	aacataaacc	ataggctgtg	720
ctccaaaggc	atattgg					737

SEQ ID NO: 10,498

ctgtacgtta	caagtttggg	cattttgaag	cttgacattt	tagtttgcca	ttatgttaaa	60
aacatctaaa	taggtgttag	tttctcagga	gtagattgtt	agtgttgact	tttcctgtaa	120
agcagacatc	gttccttggc	tgccctgcat	tgtatactag	atttcattgt	tgtctctcat	180
gcttcttgag	ttgcttcatg	gtttatgctc	gcatatgaaa	gctatcagta	acagtttcat	240
gcttatacca	aagaattaaa	tctgatcttt	aatatctgat	atcttctctg	tactcgtact	300
gataagggat	tattggaagt	cagtcacaga	atcttggaat	aaattctagt	ctctccttag	360
ctatttgatg	cttttcatat	aggccaagaa	ctcattgcaa	aacatttttg	caaggatgaa	420
tgctgtatt	tggtctagga	acagtacatt	ttagtctgat	ttagaattac	tggtagctta	480
ttttaaagca	agggaaaagca	g				501

SEQ ID NO: 10,499

ccacaagctc	tttagatggg	tacttttagt	aaactcttca	ttcatcctgg	cattcttgaa	60
aatattcgtc	aaacatagag	gaagactcat	cttcacgttc	ctttgggtct	ttaaattcta	120
ggcttctctc	atattgaatg	gcaaaatcaa	tatgctgcaa	tacaatgttc	atgctttctt	180
catctgactg	atcgtaaagg	aaaaatcgaa	ccatgctgta	gtcatcaatc	agtccacata	240

tagcttttagt	cagtttcttg	aattttttgc	ttcttaagtc	acttgtagaa	tcttctaata	300
aagaatacat	gtctggatct	aaaaatttct	caatttcctt	ttttgctttt	ttactcagca	360
gatccatttt	tgctcatgat	ttgacttgcg	gaattttctag	agagatcatg	gcactcaggg	420
ctgccaaagt	gccagaaata	aacttgaatg	actccaccat	gaactgagaa	tcaacaagaa	480
aaactccaca	gactcggaac	tcccactgct	cgagctgctg	gaccagct		528

SEQ ID NO: 10,500

actaaacagc	caatcatggg	attcaaagga	cacogtaaag	cagtctctta	tgcaaagttt	60
gtgagtggtg	aggaaattgt	ctctgctca	acagacagtc	agctaaaact	gtggaatgta	120
gggaaaccat	actgcctacg	ttccttcaag	ggcatatca	atgaaaaaaa	ctttgtaggc	180
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ctaccagatg	gggagtccaa	tgtgctgatt	gctgctaaca	gtcaggggtac	aattaagggtg	420
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SEQ ID NO: 10,501

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cagtttgctc	tgtttttagac	aaatacttca	catgactgat	gtaaactgtt	gcatagtttc	300
acaaaggctt	tctcattcat	tcttgaaatt	ctccatcagt	cacaaacaca	aattgttcag	360
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caggggaagt	attgaaagtc	attgaaagtc	atccccacc	actagaggag	agaaangcaa	480
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SEQ ID NO: 10,502

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SEQ ID NO: 10,503

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agatccctct	ttggagcttt	tttgcatagc	aattaaagg	gtgctatttg	tcagtagcca	360
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SEQ ID NO: 10,504

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218

SEQ ID NO: 10,505

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agaaggtgga ggcaccaggc tcaaaagagg aaatttasaa tytctcattg ggagagtaag 180
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SEQ ID NO: 10,506

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SEQ ID NO: 10,507

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SEQ ID NO: 10,508

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ccatatattt 610

SEQ ID NO: 10,509

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 aaatcatttt 730

SEQ ID NO: 10,510

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 ctcatgaaga agctttgcgt ggggcccacc agtgaagaca tcctcctgaa gagtggtttt 360
 ggaccagatt gcatagcaat agggcctttc attggctctg ccgggaaagt cccattttact 420
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SEQ ID NO: 10,511

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SEQ ID NO: 10,512

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 gaaacatctt cccaacaaaa gaatgaagaa gacattgaaa ttattccaat ccaagaagag 180
 gaagaagaag aaacagagac gaactttcca gaacctcccc aagatcagga atcctcacca 240
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SEQ ID NO: 10,513

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 ccca 364

SEQ ID NO: 10,514

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SEQ ID NO: 10,515

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acaaggccac	actggtgtgt	ctcataagtg	acttctaccc	gggagccgtg	acagtggcct	240
ggaaggcaga	tancagcccc	gtcaangcgg	gagtggagac	caccacaccc	tcc	293

SEQ ID NO: 10,516

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actgtatctc	cgacagatgc	agacagggtg	gaaggagatt	gggtcatctg	gatgtcacat	300
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SEQ ID NO: 10,517

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SEQ ID NO: 10,518

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ccaagaagag	gaagaagaag	aaacagagac	gaactttcca	gaacctcccc	aagatcagga	420
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SEQ ID NO: 10,519

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SEQ ID NO: 10,520

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gaaattattc	caatccaaga	agaggaagaa	gaagaaacag	agacgaactt	tccagaacct	180
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SEQ ID NO: 10,521

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cag						603

SEQ ID NO: 10,522

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gactcccaat	attgtttccc	ccacaggtaa	tcttggccgt	ctttcctggg	gccactgaca	180
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SEQ ID NO: 10,523

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SEQ ID NO: 10,524

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SEQ ID NO: 10,525

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SEQ ID NO: 10,526

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SEQ ID NO: 10,527

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tgaggagagc	aagaacaaga	tttttggcag	tcttaccttg	tgtcatgcat	ctgaatgctt	540
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SEQ ID NO: 10,528

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tactcccaat	attgtttccc	ccacaggtaa	tcttggccgt	ctttcctggg	gccactgaca	180
ctgaggggtg	ctgagtcaac	acataggagg	tcacagagtc	tgtgcagtga	gagaggaggc	240
cgaggaggag	aacggtccag	gccatggctg	aggcaccac			279

SEQ ID NO: 10,529

cctcctgctg	ctcctgtttg	tgggactggt	catctcctac	gtgatgctga	agagcaagag	60
agtgaccaag	aaggetcagt	gaagggtccc	cagggatgag	gctgccagcc	ccttctctgc	120
ttccctccca	gcacagggac	caagtggggg	agcctgcaga	acctgtccag	gcacagtggc	180
tcctcaagcc	tgctgtcctt	gcagagtccc	catggcatgg	agcttacacc	tgactgactg	240
gagccccctc	ccgactccc	acttcagaaa	gctaggaggg	agggatacct	ggaagactcc	300
ggtcacctcc	ttcttgctca	gggcctaaaa	gatgctggtc	ctcccaacct	cactctcaga	360
ctccctgcca	ccttttcccc	tgggttctgc	cgtcttgctt	cacttccctt	cctgtcacat	420
gctgacgttg	gacttagcag	gttctaaagg	cacatgtgtg	acctctctga	cttctcttcc	480
tccaccaagg	cagctttcct	tacctgaca	cagccccaga	ccccacaaag	ccttmtggac	540
ctggaaagcc	tggggaaggw	ctgacagacc	ccaggaccag	ccctggggct	cagggcagcc	600
accccgggcc	gctgacygac	tgacctctcc	tcacggaggc	ccagcccaa	agccccaggg	660
ctggcccgtt	tgggacag					678

SEQ ID NO: 10,530

aaatatggtt	gtacatgtca	tcattaatcg	attcattggt	cttccacatg	gttattttcaa	60
tgcaagatcc	gatcagcatg	aagagtctag	tacaagatag	gcagacatgg	ttatcactct	120
gcatcaccag	tcacatgggt	acagaaaaca	gaattgggac	tgcataggga	ctctactgcg	180
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attctacaat	tgaaaatgcc	tcatttttacc	ttttctctaa	actgacaaat	gcaagtagcc	360
agtaactgta	ggcttagaat	tttcggtcac	tgaccagaag	gactaatagg	cgtctatgtg	420
ctcagaacca	ccagtcccgc	accaactctc	ctttcagtga	gcaactgtcag	ccaca	475

SEQ ID NO: 10,531

acancctgac	catnaacagg	gnataaacgg	gtcgatgagg	ccgactatta	ctgtcaagtg	60
tgggatcgta	ataatgacca	tgtcgtcttc	ggcggaggga	ccaaactggc	cgtcctaggt	120
cagcccaagg	ctgccccctc	ggtcactctg	ttcccgccct	cctctgagga	gcttcaagcc	180
aacaaggcca	cactggtgtg	tctcataant	gactnctacc	cgggagccgt	gacagcggcc	240
tggaaggcag	a					251

SEQ ID NO: 10,532

caacatgcct	tctgcatctt	ttaatactac	attcacctga	ttataaatct	ccttctcaga	60
ctctgtaggg	tgggcatttt	caaaatcaag	gaaaaaat	ggcccctgct	caaggtctgt	120
gcatgtcaaa	actttaagaa	gattcccat	gttaaggtag	cttcagccag	ygctggbgat	180
tctgtccttg	bccttctatc	cttggtattg	cgttccctct	ttcctagtct	acttgtttcca	240
gtsetttcaac	ttctg					255

SEQ ID NO: 10,533

aaacattcaa	tttattttgtg	gcattttgtac	atgaaaatta	tatgacgata	acattgcttt	60
ctatttctaag	ctagtaaat	gttttctaaga	aataatagat	tgataaaaatt	gcaagtctta	120
atacaaaggt	aggttatgaa	aatgtatatt	aatttgagat	atagaaaagt	tttcaaataa	180
taatgttttc	aggttatat	gcaaatagac	actaaataag	acaagggttc	tgcaaacatg	240
atgtaacaat	aatgactgga	actctgaatg	tgggaaattc	agaaaatgaa	ccagctactt	300
aaaaagcaaa	aatgtgctaa	gtaaattttgt	atrtttcatgg	ttatttctaag	gagaggagga	360
ataatctggt	gaggttagtg	ccctcaagca	gaccccataa	ctttgctaca	ccgcatttaa	420
cttctctgtg	ctgtttttctt	ttaatttttca	aaatggaaat	tagctgtttc	attgggtgaag	480
tgcattgtaa	aatgagagaa	ttttcaaata	atgcaattac	tctatgggtat	tctgtttttaa	540
tagtaatata	cccatatgaa	gcaggtataa	tgagaataaa	ttttgcccac	aacaaattct	600
gaaatctgaa	gttttggttc	tgctgttata	gtatgaattc	gcttt		645

SEQ ID NO: 10,534

ccaatcatag	agatatctgc	accggcctgc	aaagctttcca	tgaacgcttt	ggtcccagac	60
ttggcgatag	taccaagggt	attgatcaag	tcagccttgg	tcattccaat	tccagtatcc	120
acaatagtga	gagttcgatc	ttgtttgttc	ggtataagg	taatatgcag	ctcttttcca	180
gagtctaatt	tactgggac	tgtcaagctt	tcataccgga	ttttgtccaa	tgcatctgat	240
gaatttgaaa	tgagctctct	cagaaagatc	tctttgttsg	agtagaaagt	attgatgatc	300
aatgacatca	actgggcaat	ttctgcctga	aaggcgaacg	tctcaacctc	ctcctctctc	360
atcggttggt	cttggtgtctg	ggtttcctca	ggcatcttgg	ctaagtgacc	gcacaggacc	420
aacggcacag	cc					432

SEQ ID NO: 10,535

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tggggatttg	ggaactgagt	ttttagctct	gtgacacaca	acataaaaaa	caaaaatcca	120
gtctcattag	ctaaattcgg	attaaaaatc	gaaatgtttt	tatggagtgt	ccaacaggct	180
ggaatgtacc	tgatacagtt	taatctgctt	ttattttctt	ggctgtcttc	caaaccactt	240

tcttctgtga attcttaagt tggctagtcc tcttctctca gaaaaattac ccctaagaat 300
 ctctctaata gtgaggggtgt acttccgaat agaagagtcc ttcggctgaa atggcatctc 360
 caagg 365

SEQ ID NO: 10,536

ccatgggaat ctaattaatt tcataatgat gttggttgaa catgatacca aaaaatgcag 60
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 gagaaaaaaa ggatgataaa acttaagctt ctttttcaga tgtttaaaaa tttctataaa 180
 attctttgtc ccaagattaa tcatataacc atggtacata aaatatgcta actacattgc 240
 ctggtgtcaa ggtgggaaaa tcctctttta taacataaaa tcctcttcta atccatgttg 300
 acccaagtcc tggctgtctg agggcagatt cctgtcaaga gacctaaggt tgtcatggaa 360
 agcatcactt tcgtctacta gttggtaatc ctgttccatt tccgttagga agccactccc 420
 agatcctgrc cagagcckga gccggagccg aagcctgata cagagtagtc ctcakaaagt 480
 ggaagatac gattcaagtc ctgattmtc gc 512

Sequences Listed in Figure 6-Highly expressed in lymphoma cells

SEQ ID NO: 10,537

aaatatgaat ttgtcttaaa ggcaattcct ttttgcctct gtattatctg gaaaagcatg 60
 agagaggcga cactcaaca aactgatcag agaaaataag cagttactac cctgataggc 120
 accttcccaa tctgtttgct tttgaccatt gtctgtccaa cggacacacc tcaaacaaac 180
 aaaactacca aatagatgac agatcagaat aaagggtgaga ggtctggtcc ccattgaagg 240
 ctgctacagt cttcaaagag gtgaaggagt tcataagaga acaacagtag gaaagttgag 300
 agccaagggt aggagagktg cccaaaagac tccccctact actttagggt actgaaaact 360
 caaaggatca gctacagctt tatctaagta tttactaaat gctacatgag ggtgtccctg 420
 tccagctttc tggcacatga gtctgtgtg gagagttacc tcctcttcca gggactgtgc 480
 tgttgggaac tttgggcaag tcacttacct ctttgtgcct caatttctgt ataatatctc 540
 taagctacct cactgaggtg gtatgaagat tcactaatgt atgtggcgtg tttgtcaatc 600
 ctccagtga aagcactatc tagatcacat tttggatcac attagccaaa tgcagtaaat 660
 gg 662

SEQ ID NO: 10,538

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 atgcatggaa ttattttcaa gacccgggt atgtggtctg tgggtggtg tctccctgtg 180
 attatggact gagatactca tttagtccca ataagaccag agaagtacat tgtgagatac 240
 gtgggaaacg gctgcatcac tcactgtctt gtgcatgtgt ctccccagg gcattttcag 300
 atttctgcca cggaggggat gctcttcgag aaggagagt caggtacatt ggaggattca 360
 ttgctgtgg 369

SEQ ID NO: 10,539

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 cctttttagt atcaaatttc aatcttggcc tcactggaac catgctctac agagctttcc 120
 caacagttta gcaagtaagc aaaatcagct tttgctcttc atatttcgta ggtgagactg 180
 gggctttt 188

SEQ ID NO: 10,540

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 tgtgaagatg gctgcagttt tgataccctt atcttcattt ttaggttcct gaaggaatga 120
 accaactgtt gacaacattg gtttgactac gaattgacaa cgttcttttc tagatggcaa 180

ggtaagtgtt accaagggaa ggccatgtct ataattaact gttatttcat cag 233

SEQ ID NO: 10,541

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 tgtaaggta ttgcaagaat gccaaccct ctggtgtctg atcatgtatc tagcaacatt 120
 gcagtatgaa gaaaagagat gcccggctc cagcccatgg actagttaat acagtgaagc 180
 aggttcctgt cttttaccct tcctgctcag aacataaaaag attaaggact aaaatcaagg 240
 aaggctggga gtttttagagc tggcaaaaatg aagtctaaaa gataaatcaa ggcaacaat 300
 tactgagaac ttggctgttg cttaacctgg caagtctaaa agcctttctt taaccttgta 360
 ggaattagat gcataagggt tgctgcaaca tgttcatggt aaacaaacta agtagagctc 420
 ttatttacia accttgtaac aaatacttct ggaggaaaaa gagaaaagaa ttcactaagt 480
 tccanaagac aaagctntaa ttgccagacg tatacaaac 519

SEQ ID NO: 10,542

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 aagaagaaat gtttatcaga ttttgaatga catagctgta agttggcggg tggcagcttt 120
 ccacataaaa tttcatcaga aagtgaact tgattacagc ccaaactaga caaggcaatt 180
 caggtgcccg gaccccggaag tccacgtgag actacaggag aacgtgcatt atggtgcttg 240
 ccagccagtc tcttgaggaa ctgctgttaa cggtcacggg tgtggggaga acaactcca 300
 ttttttttaa gttttttttt ttatggtatt aaatataagt cttagcacct ttggcatttt 360
 tgtccaaaca gacttcgaca tatgaagtgg ggacataacc ctcttcacat tcatctctcc 420
 gaatgcgggt ccagccatcg cctttgtctt cctctatgac atacaatgtt tctccttcaa 480
 ctacggaaat cgctccttca ttctgacctt caaatgtgta gagagctttg cacgtcccta 540
 tggcaggagg gggctcctca tcatcaaact cgctgcataa atccgtgg 588

SEQ ID NO: 10,543

ccaaaaactg gagtgtctgt ggaaacgcgt tctgccaggc tgcacagcca caaccaaatt 60
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 ctacgacctc ttgtccctt gagctcagtg aattcccacc aggtgccac agctcctgga 180
 cttcaaattc tatatattga gagagttgga gagtatatca gagatatttt tggaaaggag 240
 ttggtctatg caatgtcagt ttggaatctt cttgaaagtt taatgttttt attaggagat 300
 tt 302

SEQ ID NO: 10,544

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 ctagtggcga caaagtccag cttatgccgc tgtgagcctc tatttgaata tttgttgcaa 120
 atgcttgat gccctcattt acaagcgatt ttaattactc tcatttaatg gaaacaagtc 180
 ccaggaaaa gaaaaagaag aaaaatgata cagcaaacca tctgaagcaa tccaagtcct 240
 atgcttacag tgaccaggt ctactttgct cgaagagAAC actggtactg cattcaaacc 300
 acaacagaat ccgtcactta actgacctt ctgaattaaa ctgaggtatg aatcaatttg 360
 aggtatgaac agggaaggca aaatgcaata ccagattatg aaaataacca aaatggaaaa 420
 atttgatgta gaagatatgt ggcttggatt gctccacatc tttggttaaa acatattaag 480
 aaaagccttt aattacatct gtagtctgaa gcattctaac agacaccagt attccagcaa 540
 tcttcaaaaag atctgtagtg gcaggaaatt aacgccataa aag 583

SEQ ID NO: 10,545

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 atgagagcat gccaaaattt gctaagtctt acaaatgata agggctgtcc gcaacaggga 240
 agaacagttt tgaaaattta tgaactatct tatttttagg taggttttga aagctttttg 300

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 ttcgagtctg agttt 375

SEQ ID NO: 10,546

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 aactcttggt cacataaaat tgagttgaag ttcattgtgc ctttttttct ttatccaaat 180
 tttgagttaa agcttcatat ggtaactgca tcctgttcgg acactatagt cttaaattttt 240
 gaaactgtgt ggtgttcgct aaaagtagga ataacaacgt aaaagctaata taagggtcaca 300
 aacttcagtg aaacccttaa aagtcctaaat cttcttgata ttgtgaaccg tacccttcc 360
 agtttagttt cttctggact ttccttactt aactgacagt tacctttt 408

SEQ ID NO: 10,547

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 acttgagcaa ggacaaaaaa ttagcccaat ttaacaactg gtttacctgg tgtcataatt 240
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SEQ ID NO: 10,548

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 aaagagaaat gagggactga tacatgctaa agcatggatg agccttgagc gcatttttgc 120
 caagtgaag aaggcagaca caaaaggcaa cgtattgcat gagtgcattt atatgaaata 180
 tccaaaatag gcaaatccat ggagacagaa agcanataaa tggttgtaag aagctganag 240
 aaaggagtgg ggagagatng ctaaaaagga gtttccttct aggggtgatga aaatgttctg 300
 gaactactta ttggggatga ttgcacaaca tgggtgaagg actcaatgct nctaattgta 360
 aatttcacat acactttacc ataattttt 389

SEQ ID NO: 10,549

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 ttccatttac actgcattct tcaaatgtaa ttttcaaaga tgccttttgc ctcatccctt 120
 gcttttaagt attattatag acttttggaa actcacgaaa caagcaatcc cttaaattctc 180
 gccaggaaga gtatcttggg ttaaatgggt tttgagaacc ttgagagtgt atattctatg 240
 aaatggaaga aacaagaact agacagagtc acaaatgctg ttgatcacag acaatctctg 300
 ccatccataa ggtaaatgta atacatctgg cgacctgctg agtgtgaact tgcagcag 358

SEQ ID NO: 10,550

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 gatcgaaccc acccccacct ctagagtttt tggctgtttt cttaaagtctt gaattcaatg 120
 aggtgaagga ggaagaaagt gtttaggaag tcagtgggtt ccagaagagc tgggtgctggg 180
 tggggcagag tggtagagaga tgctcctttc aaatggaagg ctctggaacc cgccaaaagg 240
 gagtgaagc tggggcaatc ttcttggaac gccaccagag aaaggcgtca gacccac 298

SEQ ID NO: 10,551

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 aatgtacaaa ctctaagct tctaaagga ggcatggcaa aaacgttggg gtcaggatgt 240

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SEQ ID NO: 10,552

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aatgaaagt atacttttta taatttttct tttt 274
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SEQ ID NO: 10,553

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cag 363
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SEQ ID NO: 10,554

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atgatgaaac ctgcagccaa cactgccctc cacaagggtt tctggaaagg ctgaagctgg 180
agacggtaaa ccacaacacc gtcccaggtc actccaggtc accccagcta aagacattca 240
acaccagcca aaaggctaaa gtttagtttg aagggttcaa aggcaaatac actgaaaccc 300
acgtgtaaac ctgcctgggt ttcaaactgg aagagaaaca ctttggtgtc ttcaataacc 360
cagg 364
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SEQ ID NO: 10,555

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ccaaatctct tatccaatgg aggtactgag tggctggatc agttaccatg caagctcacg 60
atgaatgaga ttgaatttgg ttctgtgtgc acactgggct ctggggagggg aggcaccccc 120
tgtgtgttgc tgctgccttc cgtgctgtct actgtatcct tcatgtgtct ccaaattggt 180
cacgccccat gggattacag aacacagcta cagaattagg atctcatggt aacaatgagg 240
aattagggtta ctgtagaact aaaatatgtt taatgaaatt aaaatgcaat ggaaaaaaaa 300
tcaggcaaca gaacattctg atgaatttac aggactgatt atatcccacg gcaactgaatg 360
acaaacagtt cttctccata cagtcgcaat tagaggcata gaagtcatac tgaatgctga 420
atagaagaac actgagaaga gcagggtata aatgaagggt ttcacattaa acagaaaaat 480
agacaaaatc atcggtaaga agctagctt 509
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SEQ ID NO: 10,556

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aaacagcacc agcacttctg gctggtttga accttaaagt ccaccaccca ccagagagga 60
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cagaagaaac ttattagaat aaggccacct aggaatgttc ttaacttttc cattcagctt 180
ttggctgata tatgaaaata caaataaata catcctttcc ccaggtgcaa ggctaaacca 240
gcagctccaa gggcttggtc tacagtgtc agaaagacac actgccttaa aagtcaggct 300
agtgccctag ctccgggtggc ctctgcaaat gagg 334
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SEQ ID NO: 10,557

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ctgttctccc ttgaggacct ggtcaggatc aagaaagggc tgctggcacc cttactcaag 60
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tttatttgtg aattttgccca gaatacgact gtcatcttcc catttcagac agcaacatgt 180
agaagatgtt cagcgtgcag ggcttgcttt cacaaacagt gcttccagtc ctccgagtgc 240
ccccggtgtg cgaggatcac agcgaggaga aaacttctgg aaagtgtggc ctctgcagca 300
acatgatgcc cctgagtact gtgaaaaaga ctgttcaaca tgccttatga taacaccgat 360
ttgtgtctat tattgggtgac attgttttag atattgggta ttgtatatta aggaaaaaga 420
tgggtctatat tctcttttatt gcatatactt aatgtttcaa aagaatgcag attctgtgtt 480
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tttttt                                     546

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SEQ ID NO: 10,558

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aattttctac ggagaagggt aaagtcaatg gcaaaactgg aaatctcggg aatgttggtc 180
acattgaacg cttcaagaat aaaatcacag ttgtttctga gaaacagttc tctaaaaggt 240
atttgaaata cttaccaag aaatacctta agaagaacaa tcttcgtgat tggcttcgag 300
tggttgcatc tgacaaggag acctacgaac ttcgttactt ccagattagt caagatgaag 360
atgaatcaga gtcggaggac taggcaaagg ctccccttac agggctttgc ttattaataa 420
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SEQ ID NO: 10,559

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tacagatgtt ttaccttaag aattatttaa gttgtgttgg gttaagacag ttttcagtgt 180
accgtaaatg ttgtgttttc agaaaaagac aaaacgatgg tgctgactgg ttttctgtat 240
attgcacaac agtcctcaaa tacactgatg tatgaaacta ttcatacatc aagcagcatt 300
tttttctact tccttagaat tggaaactat cagttaaggc agataaaatg tacagatgtt 360
tcatatatta caggttacat atataaatca aaatttccta tataaaactg atttggggatt 420
tgggggtggaa atattttgaa tattaattta ttttt                                     455

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SEQ ID NO: 10,560

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ccacagcatc cccacgttct gagaagtact tggaaatggg tgtctggaaa gcttccactt 60
tggctcttgac ggcattcacc ctctccagca ccttctcctg gattgctacc ccaaaatcat 120
ttccatcttc aatcttgggg atcagggtgt ggatccatgt aatcaccaga atgcatttct 180
ctttgagagt ccagacttct ggcttaacca gggcaagcag ggacaggact ttctcattcc 240
cagggagaaa tccacactta gggacttctt tcttctcctg cttatctgtt tccatctcat 300
catccttggg tggagggtct gggatgggga tgtccagtgg ggcccggagg gaagtcaagt 360
cagccacatt gagggagtcc tcttgcaaga gctgattcag gtatatgatt ttctgtggca 420
agaatctgta gaggaattcc tcagcctcct ggaaaagatt ctgcctgaag tctctcc 476

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SEQ ID NO: 10,561

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aaaatgcatt ttcccttgtc ctgtctttta ctagatatac atgcttatat ttatagtggg 60
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gaagatattt ttggagtaat ggtgctgtct tgtagcgagt tattaatcat agtaagattt 180
tttctcttc atttctttt atttctttt attaacaatt ttttttttac acggacacaa 240
ccctctgaca gtcttttcaa atattaaaat tctttgaata tgtatgctgt gatctgaaca 300
ctgctcaagc catcaagcag tcttcataca gtttgcatta taaaatctca tttaaattctc 360
caagaaaaaa taagttgaag aattttattt cctgaccatg catcccctgg atttctgagt 420
ttcagttcag attgtagatg acaatataag ctgccttcgg aaattgtcaa catctgaatg 480

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ttaagtccat tttcccatg gaagaagccc gtagttccat gaagtatgga ttaccatttg 540
 tattttttcac taacagtaaa tgtatttttc ttattaattg tttgccttag gaatgatgaa 600
 ttacattttt tgttccttct taccataaac atctgcattc ctcagctcag ccttccttgt 660
 atgttgtttc tttataaatg gttgagctgc tgatgcaggt attcccaagc tancagtaca 720
 aatcatttt 729

SEQ ID NO: 10,562

aaaatatattt aatcaggcag agttttatgg atagagaata gaagagaaaag gtagtaaata 60
 ttgaacatat tccaatatag gaacctatct ctgttttagt acaaaatatt tctgacatct 120
 gaactagagg tcaagagaat aaatttcattt gtatacatct gagcaacctg tctttcagat 180
 gataaagtat ctagcctttt ctgacaccat aatagttcat tttgtaggga ataagccatt 240
 aggtgtatat aattgctttc tagaaatgac ctaatgtccc caaccacttt gtagtggcag 300
 atcactgttt cacagcatat tttctcccaa ggaaagtatt caaaagagac tgcaactaac 360
 annactctta tttcatcaaa attt 384

SEQ ID NO: 10,563

aaaagagcaa aatgtttatt ttttatatat cttcttagat gcctataaaa ctacaaagaa 60
 aattacccta ttccactgaa aaggagagca gagaataaat taaacctttc tactatatgt 120
 gccttttttt caactatgct aacttaatgc tgtacatgta atttcacttt tcagattaac 180
 attgacagtt cgacaagaga gactatcatc aggaacattc aggaaccacac tgaaacatgt 240
 tttgaagaag ctcagaaaat agtctatatg catatggaaa gggattccta cccagattt 300
 ctaaagtcag aaatgtacca aaaacttttg aaaactatgc agtccaacaa cagtttctga 360
 ctacaactca aaagttt 377

SEQ ID NO: 10,564

aaaagtattt tctctacaga gaatcttatt agctatacaa aaatntgtac agtttttata 60
 ctgaagctag tattgagctg cacttgaatt cacattctta gcaaaataat tgccctgagca 120
 cacacacaca ttccacacgc atcattaaag gatagccatt tattcttcat cttcactctc 180
 ttctctctca tcttcatctt cttcttctc ctcctcctcc tcatcttctg gttcgttctt 240
 cttctttgag cctgttgagg tgccagggcc cttctttcct gcttcacttt tgcccttggc 300
 acgatatgca gcaatattct tttcatattt ctcctttagc ttagctgctt tctgttcata 360
 tggntgttta tctttggctg actgctcaga ccacatttca cccaatttct ttgcagtatc 420
 cccaatggat aggccagggt gttcactttt gatctttggg cgatgtt 467

SEQ ID NO: 10,565

aaagaacaga gttctggagt aaagaagcag gttccctttt cagtagacac ctcccgtctg 60
 ctggttgaac acatcaattg tatcttcatt ctcattttcc aactgtgcag gtgtgtctgt 120
 ttcattgatt gggtgcccgt caaatcggaa tntgatctgc ctcattgaca atccctgtcg 180
 ttcacaatag gccttcatta gtttactaag tgggtgatgc ctcttaatct taaactgcac 240
 cacagaacca tccctgcccgc ccacctcaa attaatatga tcgttggtct cagtcttgac 300
 tctttccttg ggcttttctg cggccatggc gagcgccgga gtctctcag 350

SEQ ID NO: 10,566

ctgaagctgc aggtgctgat cgagtcaaag agccctgaca tagccatgct ttttgaagaa 60
 gccttttgtgc acctgaaacc ccaggtttgt ctgccattgt ggatttccctg ggcagagtgg 120
 agtgaaggtg ccaaaagcca agaagacact gaggcagtct ttaagaaagc tctcttagct 180
 gtcataggtg ccgactcagt aaccctgaag aataagtacc tggattgggc ttatcgaagt 240
 ggtggctaca aaaaggccag agctgtgttt 270

SEQ ID NO: 10,567

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ctgcctataa aactagactt ctgacgctgg gctccagctt cattctcaca ggtcatcatc 60
ctcatccggg agagcagttg tctgagcaac ctctaagtcg tgctcatact gtactgccaa 120
agctgggtcc atgacaactt ctgggtggggc gagagcaggc atggcaacaa attccaagtt 180
aggggtctcca atgagcttcc tagcaagcca gaggaagggc ttttcaaagt tgtagttact 240
tttggcagaa atgtcgtagt actgaagatt cttcttttcg tggaagacaa tggatttcgc 300
cttcactttc ctgtccttaa tatccacttt gttgccacac aacacaatgg ggatgttttc 360
acacactcgt accagatctc tatgccagtt aggcacattc ttgtaagtaa ctctcgatgt 420
tacatcaaac attatgatgg cacactgggc ttggatataa tagcc 465

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SEQ ID NO: 10,568

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ccttgatgat accattatcc tcattataga tgatgcacgg gcccctgcgc tggatacggc 60
gacggttttct cattttgcct ttgccagctc tcattcgctg agaggcatag acctacaaag 120
tgagcagttt tagtattctg attaagatag aatctctgca atagatcttc agagttttaa 180
ttccttttta cagatgatta aactgggcac aataacttgc caaggttaca cagagccata 240
aacagcagtt aggattcaaa cccaagtaat cgggctctga ggttcttggt ctctcacaca 300
ttaaggctta gctatactgc ccttatcttc tgaaattcaa agtgacaaac tgtgaacaag 360
gagtacaaa ctgtaaagt gctcattgaa cggacctttt tgatatcatt ccaggcttta 420
agtttcttaa ggagcaaaac agcttccttg gtcttcttgt agccttcaac tttatcttca 480
actaccaag gaagttcagg aacttcctca atacgatgac ctttagacat gaccagtgtc 540
ggtagggctg aggcagccag ggcagaacag atggcgtatc gtttttgggt tgtgttcact 600
cyacgatgcc aacggcgcca ggttttgggt ggtgcaaaca ttcggcctcc acgacacatg 660
tttccaaaag caccctgg 678

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SEQ ID NO: 10,569

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cgccaatctt cgctctgagg tgctgtctca ccggtgagac ctggaagcgg gcgagtctcg 60
tgctgtgtcg gacctgcagc ccctggcctt ccgccaccat ggagtacctc atcggtatcc 120
aaggccccga ctatgttctt gtgcctccg accgggtggc cgccagcaat attgtccaga 180
tgaaggacga tcatgacaag atgtttaaga tgagtgaata gatattactc ctgtgtgttg 240
gagaggctgg agacactgta cagtttgtag aatatattca gaaaaacgtg caactttata 300
agatgcgaaa tggatatgaa ttgtctccca cggcagcagc taacttcaca cgccgaaacc 360
tggttgactg tcttcggagt cggaccccat atcatgtgaa cctcctctcg gctggctatg 420
atgagcatga agggccagcg ctgtattaca tggactacct ggcagccttg g 471

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SEQ ID NO: 10,570

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ccacatatgc ccctgtcatc tctgctgaga aagcctacca tgaacagctt actgtagcag 60
agatcaccaa tgcttgcttt gagccagcca accagatggg gaaatgtgac cctcgccatg 120
gtaaatacat ggcttgctgc ctgttatacc gtggtgacgt ggttcccaa gatgtcaatg 180
ctgccattgc caccatcaaa accaagcgta ccatccagtt tgtggattgg tgccccactg 240
gcttcaagg tggcattaat taccagctc cactgtggg gcctggcgga gacctggaaa 300
tgttcatgaa tgtttgaaag gaacaaaatt atcagggatg gctctttgcc atgggtctta 360
ttttcaccct cttttctgta agaaaaaaga acaatgtctt aatgtatttt t 411

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SEQ ID NO: 10,571

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tttttttttc caagtaagcg tctatgcagg catcacaaac tttggcggat acagtagata 60
tgtattttct tgatgctgaa aggtcagtc ctaagacaaa atcaaagtgc tcaaagaatt 120
aaaagcaaaa tgcattgtgc ttcttggaag aggtttccat ttgcaatgta atctgcattt 180
ctacaaatac tcaatgtcca aggcactag agggtgaaaa accagggcag cgtcttccag 240
caggggtcag ggcagaccca gagccaaaac tccatcctca gcccaacctt ggaggcccag 300
cag 303

```

SEQ ID NO: 10,572

aaattgatct	ggtgttcctt	gcggggcttc	aattgcattct	aaataratgt	gagagttgaa	60
agacccataa	ggggcttctc	tcgctttacg	atgtcttatt	atTTTTTTTT	ccttcctctg	120
gttgatgaaa	tgccaggggtg	aaagggatag	ccaaataggc	taaagcaca	gtgccactct	180
agttattcsg	cagagtgtccc	aataaagggtc	cacgacaata	ccatcacaca	tccgctcggg	240
gatgaacaag	ggctgactga	ctgataagyt	cttgaaaatt	cttaagctca	ctgcatccct	300
tcaggtctcc	aaggaatgct	aagtctcctc	cctgccatga	gagacatgaa	atgaacttag	360
tgttggggaga	cggaagctgg	acggccctca	ggggctgacc	cgcagggact	ttgggatata	420
gcagagagag	cttggtcatga	cttattactc	caagctgtag	aaacctggaa	aatagctacc	480
ctgcagccca	tgcttggtca	actggaggac	caccttagtg	gaagggggac	aatcagggcc	540
tctggcctgc	catgtgcaca	agcataacaa	ttgcatttgt	tt		582

SEQ ID NO: 10,573

aaagaacaga	gttctggagt	aaagaagcag	gttccctttt	cagtagacac	ctcccgtctg	60
ctgttggaac	acatcaattg	tatcttcac	ctccatttcc	aactgtgcag	gtgtgtctgt	120
ttcattgatt	ggttgcccg	caaatcggaa	tctgatctgc	ctcattgaca	atccctgtcg	180
ttcacaatag	gctttcatta	gtttactaag	tggtgtatgc	ctcttaattct	taaactgcac	240
cacagaacca	tcctgccccg	ccaccttcaa	attaatatga	tcgttgttct	cagtcttgac	300
tccttccttg	ggcttttctg	cggccatggc	gagcgccgg			339

SEQ ID NO: 10,574

aatcaataa	gtaatctagg	actagcatta	tgtttgctag	acctggcatt	tgctcggtac	60
ataaggttca	aagtttccct	tccttttttt	atTTTtttta	tattttgcaa	tgTTTTTTTT	120
ccataatatt	taagtttttc	gatgtttaga	tatttttctt	cgggtgaagca	caagtttctt	180
ttcatggtcc	ctgatcaatt	tt				202

SEQ ID NO: 10,575

ctgagaattc	gtccgctccc	gaggctgagc	agggcggggc	tgagtaaattg	ccggccttacc	60
atctctacca	tcattccggtt	tagtcatcca	acaagaagaa	atatgaaatt	ccagcaataa	120
gaaatgaaca	aaagattgga	gctgaagacc	taaagtgtct	gctttttgcc	cgttgaccag	180
ataaatagaa	ctatctgcat	tatctatgca	gcatgggggt	tttattattt	ttacctaaag	240
acgtctcttt	ttggtataaa	caaacgtgtt	ttttaaaaaa	gcttggtttt	tctcaataacg	300
ccttt						305

SEQ ID NO: 10,576

gagacaatgg	ccccgatgtt	atggagcccg	aaggcgtcat	cgagagtaac	tggaatgaga	60
ttgttgacag	ctttgatgac	atgaacctct	cggagtccct	tctccgtggc	atctacgcct	120
atggctttga	gaagccctct	gccatccags	agcgagccat	tctaccttgt	atcaaggggt	180
atgatgtgat	tgctcaagcc	caatctggga	ctgggaaaac	ggccacattt	g	231

SEQ ID NO: 10,577

cctgcagcat	gggaggtacc	acgctggcag	tcagcagtca	caccaggggtg	gtcagagaca	60
ctggtggcag	catctgtgct	tgcaactgca	ttcccagggt	gtctgttttg	ttcccaagtg	120
tctcccacaa	aattccccag	gaggttctcc	gattaaatgt	cctcaggggtg	aaaagcatgg	180
acaccaaate	actccgtatc	cacttccatg	agatgtcttg	atgctccagt	tcaatgagta	240
acaatttctc	aagaggctct	gattagtcca	ttaaaaata	agcaccacca	cctcattccc	300
cgtgatacag	cacatctagt	aatctaggcg	cctcagctaa	gctgcatagc	tcttagcaca	360
caggacaggt	cagcgttcac	acatcaacac	tataactatg	cggcggaact	agctccccgc	420
tagccgtcaa	ctactcagga	gactacctgt	gag			453

SEQ ID NO: 10,578

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aaaacggggg ggaacgggga aacgagctgt atctatgggt cacctcattc aacttccttg 60
agttatggca ctatgatgtt gcttaattag gtaagacatg gatatttgca ccgagtgcaa 120
atactgttca taacaagggtc atagctagaa agacagatgg gctcaagtgt ggacaaataa 180
tgtcatcaag gtaatagatc aaaaatatta aagccctata aaagatctga gcagtcaact 240
ccaaaacatc cacatgacaa agtccttaaa atacaaatct cattactctt actcatgcaa 300
ctgctaaaaa atagtgtgca gatatgtatt tatatttgcc ttaaccttca aaatctaggg 360
acataaatct tgctttgtta aaaaaaata aaaaataaaa atagacagga atttgctaca 420
cttttccttc                                     430
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SEQ ID NO: 10,579

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ctgctgcccc tnagtnttct ttcctttctc ttttcttttc ctttcttctc tcttgtgcat 60
tcttcaggtc agtcatcaca ttcaaagtct tccataccca cataaccaca atgatcatgg 120
cattcaccag cagtgggggt gaaaatacta tagaaatgaa catccccctg gagtccgaaa 180
tactggtatt tcgaaaataa tctccagttc atcgagcccg cctcattgat gtattcagca 240
cagtagacta agatgactag acacagaaag ngccccgatc tgtacnctgt agctncggga 300
ggacaagcag gngaggagca cgcagagccg cgtggaaggg gg                                     342
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SEQ ID NO: 10,580

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tttttccgcc catgttagca ttgaagttgt gagctctact tgcttgtctt tatggccctt 60
taattcaagt aattgggtcag tatccgtatg ggtcttttat accacccgct gggggctaaa 120
ctaatttagc tgctgctgta tacttactaa caaggaataa atgttaagct ttcttctcag 180
tattgatgga tggatatctaa aagtattttt atgtttcttt aacatggctt aaattttgaa 240
cttaatgtat caagttagta tgggtcatatt aatacctgtg cttttcagat tcttcaaaca 300
cctaaatgaa agtgataaat tcaaaactga tccttttagt tcctcattat atgatatgaa 360
gggattaact gtagcaggat agtcaacctg accgtacggc atggtgcttt ttttcaggat 420
aaatcttcag acaaaaaagt gcaaacaaaa gggaaaaggg gagcaaaggg aaaacaggcc 480
gaagtggcta accaagaaac taaagaagac ttacctgagg aaaacgggga aacgaagact 540
gaggagagtc cagcctctga tgaagcagga gagaaagaag ccaagtctga ttaataacca 600
tataccatgt cttatcagtg gtcctgtctt cccttcttgt acaatccaga nga                                     653
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Sequences with the same tissue expression profile as CD20 and CD52 and related sequences

SEQ ID NO: 10,581 - Lyl447 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,582 - Lyl448 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,583 - Lyl449 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,584 - Lyl451 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,585 - Lyl452 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,586 - Lyl453 nucleotide sequence

1005742500
202205242500

see, Figure 9

SEQ ID NO: 10,587 - Lyl454 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,588 - Lyl456 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,589 - Lyl458 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,590 - Lyl464 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,591 - Lyl480 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,592 - Lyl482 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,593 - Lyl483 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,594 - Lyl484 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,595 - Lyl485 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,596 - Lyl488 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,597 - Lyl464 full length DNA sequence

see, Figure 10

SEQ ID NO: 10,598 - Lyl464 protein sequence

see, Figure 10

SEQ ID NOs: 10,599 - 10,819 - Lyl464 MHC Class binding peptides

see, Figure 12

SEQ ID NOs: 10,820- 10,842 - Lyl464 Immunogenic portions

see, Figure 14

SEQ ID NO: 10,843 - Ly1464 - sense primer

see, Figure 15

SEQ ID NO: 10,844 - Ly1464 - anti-sense primer

see, Figure 15

SEQ ID NO: 10,845 - Ly1464 1080 bp sequence

see, Figure 16

SEQ ID NO: 10,846 - Ly1484 4141 bp sequence

see, Figure 17

SEQ ID NO: 10,847 - Ly1484 protein sequence (long)

see, Figure 17

SEQ ID NO: 10,848 - Ly1484 protein sequence (short)

see, Figure 17

SEQ ID NO: 10,849 - 10,908 - Ly1484 long MHC class I binding peptides

see, Figure 19

SEQ ID NO: 10,909 -10,968 Ly1484 short MHC class I binding peptides

see, Figure 20

SEQ ID NO: 10,969 - Ly1488 Protein Sequence

see, Figure 27

SEQ ID NO: 10,970- Ly1488 2401 bp DNA sequence

see, Figure 27

SEQ ID NO: 10,971 - Ly1456P sequence

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ggtgtgcatt atgttggatg attgtaaatt ttcagtgcaa aatgtaccgt gtcctaaatt 60
taaagacatg aaaaatatcc caagatcata ctagatcata atagcaattc ctttaciaat 120
gaattatgga ggtaactgat ctctaacagt ttccttcatt ttgttttaat gcacaagggc 180
agaggatctg ctgacccttg gaaccagcgt gactaaccac gtgctataga cacttcattg 240
tgtcgacccc aggggaagtca aagcgctttg ctccctcact gtctgtgagt cctcagccat 300
tagtacccca cccccgctg ctccaaaact tgagttattt caaatgtttc tctactgttca 360
tctctccact gaccaccact cagaaagcct ggagagagtc ccaagatgcc acccaccttc 420
cccaatccct cgccacagat ctgtgtctat ctcacactct gtaagtgccg ctttgc 476
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SEQ ID NO: 10,972 - Alternative Ly1456P sequence

aaatttagga cacggtacat tttccactga aaatttaca tcatccaaca taatgcacac 60
 caccctcaa aggtaacatt agctcatata caaaatcatg gaaaacctca caacatcctt 120
 ggaaggtaga tattgttata tccttacaaa aatttaatac acccattaac attcctattt 180
 caaatagctc aatcgatata aacacataag acagcccaca attgtgatac agnattaaga 240
 agaaactcag gccagccgag gtgcctcag cctgtaaccc caacactttg ggaggctgag 300
 gcgggcagat cacctgagcc caggagttca ggaccagcct ggacaacatg gtgagacccc 360
 gtctctacaa aaagtacaaa aattagctgg gtgtggtgac ccacgcctgt agtcccagct 420
 agttgggagg ctaagacggg aggatggctn gttgcttgag cccaaggagg t 471

SEQ ID NO: 10,973 - Ly1456P PCR subtraction library fragment

aaaataagct atggtttttc cagtagccaa aatgatcctg caccanagct catanactga 60
 gaacctganc atgcaaanc acagtctggg tgaagggatg tctgctttgt aaatgacctg 120
 ctaattcttt gcaaccacac gtaatttggt ttctgtgaac ccacagaagc agggccacca 180
 aaaagggcct tgtctgctag cctggagtat acatgantca ctggcggtgg gatcagtcac 240
 tttttaggct gccccatttt cctaacatgt taaaatgtgt gttctcagtc ttttcaagag 300
 aggaagaagc aaagcggcac ttacagagtg tgtgatanga cacagatctg tggcgaggga 360
 ttggggaagg tgggtggca 379

SEQ ID NO: 10,974 - Ly1451 240 bp sequence

cctaagccgc ctaaggggct gcctcggctg tccatcagtt acctcgtttc ctgagcagag 60
 taattgggtg agattgttca tggaggcatt gctggctctc tagtcctgga acctacagtt 120
 ggtccaattc attatgccaa agggtcctgc taggaggttc ttgttccaag tattgagatt 180
 cccgagagaa gtaggtcccc ttagatagaa gcagagtttc tcagaggtat ttagcagcag 240

SEQ ID NO: 10,975 - primer for His-Ly1452P

5' gtgtcacaaatctacagtcaggcaggattctcc 3'

SEQ ID NO: 10,976- primer for His-Ly1452P

5' gttatgtagcggccgcttatcatgttgctgcagag 3'

SEQ ID NO: 10,977- primer for His- TCL1

5' gccgagtgcccgacactcgggg 3'

SEQ ID NO: 10,978 - primer for His-TCL1

5' catttgaattcatcagtcacatctggcagcagc 3'